

AMENDMENTS TO THE CLAIMS:

Please replace the claims with the claims provided in the listing below wherein status, amendments, additions and cancellations are indicated.

1. (Currently amended) ~~Tools~~ Method for the ~~diagnostics, diagnosis~~ and/or molecular definition ~~[[and]]~~ and/or therapy development for chronic inflammatory joint diseases and other inflammatory, infectious or tumorous diseases in ~~the human~~ humans or animals, ~~whereat these tools are realized under~~ the method comprising, for humans, employment of the substances which are sequences of single genes, a selection of genes or the entirety of the genes ~~mentioned in table~~ of Table 1 and and/or of the genes coding for the proteins ~~mentioned in table~~ of Table 2 and/or employment of partial or complete sequences of single, a selection, or the entirety of proteins and peptides deduced from said gene sequences, and, for animals, employment of substances which are homologs of said substances for humans.

2. (Currently amended) ~~Tools~~ Method according to claim 1, ~~characterized in that they include~~ in which the gene sequences, ~~which in respect~~ to their sequence are identical with the ~~genes mentioned in table 1 or with the~~ genes coding for the proteins mentioned in table 2, or ~~which~~ have a respective

sequence identity of at least 80% in the protein-coding regions of, the genes of Table 1 or the genes coding for the proteins of Table 2.

3. (Currently amended) ~~Tools~~ Method according to ~~claims 1 and claim 2, characterized in that they include~~ wherein the substances comprise sequence sections or partial sequences, which in respect to their sequence are identical with ~~the genes mentioned in table 1 and the genes subsumed under claim 2, or~~ which have a sequence identity of at least 80% with the respective sections of, the ~~mentioned genes~~ of Table 1 and the genes of claim 2.

4. (Currently amended) ~~Tools~~ Method according to any one of claims 1 to 3, ~~characterized in that, they are based on the employment of a~~ further comprising

[[4.1.]] a High-Throughput method of (micro-) array-hybridisation or

[[4.2.]] a High-Throughput method using techniques of ~~[[the]]~~ polymerase chain reaction for (semi-) quantification.

5. (Currently amended) ~~Tools~~ Method according to any one of claims 1 to 3, ~~characterized in that they are based on the employment of~~ further comprising using a labeled patient sample and a second, differently labeled

control sample[,] ~~which is used~~ for a comparative double hybridisation to a ~~(micro-)~~ an array together with the patient sample to effect a ~~[[()]]~~ comparative red/green hybridisation~~[[()]]~~.

6. (Currently amended) ~~Tools~~ Method according to ~~claims 1 to 5~~ for ~~diagnostic purposes, characterized in that they are based on the employment~~ claim 1, wherein said method is for diagnosis and the substances comprise partial or complete sequences of single, a selection, or the entirety of proteins or peptides deduced from the said gene sequences ~~in claims 1 to 3~~.

7. (Currently amended) ~~Tools~~ Method according to claim 6, ~~characterized in that they are based on the employment of~~ wherein the substances comprise single proteins, a selection of proteins or the entirety of the proteins ~~mentioned in table~~ of Table 2.

8. (Currently amended) ~~Tools~~ Method according to ~~claims~~ claim 6 and or 7, characterized in that they are based on wherein the use of partial protein or peptide sequences of single proteins, a selection of proteins or the entirety of the ~~proteins mentioned in table~~ comprise partial sequences of proteins deduced from the genes of Table 1.

9. (Currently amended) ~~Tools~~ Method according to ~~claims claim~~ 6 to 8 or 7, characterized in that they include proteins or partial protein sequences, ~~which~~ wherein the substances in respect to their sequence are identical with or have a sequence identity of at least 80% with the proteins deduced ~~in table from~~ the genes of Table 1 or with the proteins ~~mentioned in table of Table 2~~ [[.]] or ~~which have a respective sequence identity of at least 80%.~~

10. (Currently amended) ~~Tools~~ Method according to ~~claims claim~~ 6 to 9 or 7, characterized in that they are based on the employment of further comprising [[10.1.]] High-Throughput methods ~~in the analyties~~ for analysis of protein expression [[()] comprising high definition, two-dimensional protein gel electrophoresis, MALDI techniques~~[[()]]~~ or [[10.2]] High-Throughput methods ~~in the~~ for protein spotting ~~technique~~ [[()] by means of protein arrays~~[[()]]~~ designed to screen for screening for auto-antibodies ~~as diagnostic tools~~ for diagnosis of inflammatory joint diseases and other inflammatory, infectious or tumorous diseases in ~~the human~~ humans or [[10.3]] High-Throughput methods ~~in the technique of~~ for protein spotting [[()] by means of protein arrays~~[[()]]~~ designed to screen for screening for autoreactive T cells ~~as diagnostic tools~~ for diagnosis of inflammatory joint diseases and other inflammatory, infectious or tumorous diseases in ~~the human~~ humans or

[[10.4]] Non-High-Throughput methods ~~in the technique of~~ for protein spotting ~~designed to screen~~ for screening for autoreactive T cells ~~as diagnostic tools~~ for diagnosis of inflammatory joint diseases and other inflammatory, infectious or tumorous diseases ~~in the human~~ humans.

11. (Currently amended) ~~Tools~~ Method according to ~~claims~~ claim 6 to ~~9 or 7,~~ characterized ~~in that they are based on the~~ further comprising employment of antibodies[[,]] which are specific for ~~proteins or~~ said partial or complete sequences ~~specified in claims 6 to 9~~ of single, a selection or entirety of said proteins or peptides deduced from said gene sequences.

12. (Currently amended) ~~Tools according to claims~~ Method according to claim 1 to ~~11,~~ characterized ~~in that they are based on the use of the~~ corresponding homologous sequences of another species for the analytics in ~~animal experiments or for the diagnostics in animals with inflammatory joint diseases and other inflammatory, infectious or tumorous diseases~~ for animals, wherein said substances are said homologs of said substances for humans.

13. (Currently amended) ~~Tools according to claims~~ Method according to claim 6 to ~~11~~ as diagnostic tools ~~for the detection of genetic alterations~~ [[()]]or

7, wherein mutations in the said genes ~~mentioned in claims 1 to 3 or~~
~~alterations in the regulatory sequences (promoter, enhancer, silencer, specific~~
~~sequences for binding further regulatory factors) of these said genes are~~
detected.

14. (Currently amended) ~~Tools~~ Method according to ~~claims claim 6 to~~
~~11 and 13 for the detection of genetic alterations or 7, wherein~~
~~mutations~~ in the said genes coding for the proteins ~~mentioned in table of~~
Table 2 or alterations in the regulatory sequences ~~(promoter, enhancer, silencer,~~
~~specific sequences for binding further regulatory factors) of these said genes are~~
detected.

15. (Currently amended) ~~Tools~~ Method according to any one of claims
1 to 5 ~~for the 3, 6 and 7, wherein molecular definition definitions of~~
~~inflammatory joint diseases and other inflammatory, infectious or tumorous said~~
~~diseases in the human, whereat these tools are realized under the employment of~~
~~the genes or DNA-sequences mentioned in the claims 1-3 or the respective,~~
~~deduced proteins or peptides and of the proteins and partial protein sequences~~
~~from claims 6 to 9 or their corresponding, coding gene sequences~~ humans are
determined.

16. (Currently amended) ~~Tools~~ Method according to any one of claims 1 to 5 ~~for the selection of a therapy 3, wherein therapies for said for~~ inflammatory joint diseases and other inflammatory, infectious or tumorous diseases in the human, whereat these tools employ the genes or DNA-sequences mentioned in claims 1-3 or the respective, deduced proteins or peptides are selected.

17. (Currently amended) ~~Tools~~ Method according to any one of claims 1 to [[5]] 3, wherein progress of therapies for ~~monitoring the progression/controlling the therapy of~~ inflammatory joint said diseases and other inflammatory, infectious or tumorous diseases in the human, whereat these tools employ the genes or DNA-sequences mentioned in claims 1-3 or the respective, deduced proteins or peptides is monitored and the therapies are controlled based on said monitoring.

18. (Currently amended) ~~Tools~~ Method according to any one of claims 1 to 5 ~~as molecular tools for the development of 3, wherein~~ therapy concepts are developed, which include the said therapy concepts comprising direct or indirect impact on the expression of the said genes or gene sequences mentioned in claims 1-3.

19. (Currently amended) ~~Tools~~ Method according to any one of claims 1 to 5 ~~and 18 for the development of 3, wherein~~ therapy concepts are developed, ~~which include the~~ said therapy concepts comprising direct or indirect impact on the expression of ~~the~~ said proteins or partial protein sequences ~~mentioned in~~ claims 6 to 9.

20. (Currently amended) ~~Tools~~ Method according to any one of claims 1 to 5 ~~and 18 to 19 for the development of 3, wherein~~ therapy concepts are developed, ~~which include the~~ said therapy concepts comprising direct or indirect impact on ~~the~~ autoreactive T cells being directed against ~~the~~ said proteins or partial protein sequences ~~mentioned in~~ claims 8-11.

21. (Currently amended) ~~Tools~~ Method according to any one of claims 1 to 5 ~~and 18 to 20 for affecting the 3, wherein~~ biological action of ~~the~~ proteins deduced from ~~the~~ said gene sequences ~~mentioned in~~ claims 1 to 3 is affected.

22. (Currently amended) ~~Tools~~ Method according to any one of claims 1 to 5 ~~and 18 to 21 for affecting the 3, wherein~~ direct molecular regulatory circuits/pathways, in which ~~the~~ said genes ~~mentioned in~~ claims 1-3 and ~~the~~

respective[[,]] ~~deduced~~ proteins deduced therefrom[[,]] are involved, are affected.

23. (Currently amended) ~~Tools~~ Method according to any one of claims 1 to 5 and 18 to 22 for ~~developing therapy concepts under the design and employment of 3, further comprising constructing and applying~~ interpretation algorithms ~~using the mentioned genes and sequences and their regulatory mechanisms, in order to recognize or predict therapy concepts, therapy effects, therapy optimizations or diseases prognoses.~~

24. (Currently amended) ~~Tools~~ Method according to any one of claims 1 to 5 and 18 to 22 for 3, further comprising developing biologically active drugs for said diseases (Biologicals) ~~under the employment of genes, gene sequences, the regulation of genes or gene sequences, or under the employment of proteins, protein sequences, fusion proteins according to claims 1 to 3 and 6 to 9 or under the employment of antibodies or autoreactive T cells according to claims 10 to 14.~~

25. (Currently amended) ~~Array as a molecular tools~~ A molecular tool ~~comprised of an array~~ A molecular tool comprised of an array, the array being

comprised of different antibodies or molecules with a comparable protein-specific binding behaviour, ~~which are intended for the detection of the~~ antibodies or molecules being capable of detecting the entirety of or a selection of the proteins deduced from the genes in ~~table~~ Table 1 or ~~for the detection of~~ the entirety of or a selection of ~~[[the]]~~ said proteins ~~in table~~ of Table 2.

26. (Canceled)

27. (New) Method according to any one of claims 1 to 3, wherein said substances are employed in connection with analysis of blood samples or tissue samples in medical diagnosis.

28. (New) Method according to any one of claims 1 to 3, wherein said substances are employed in connection with analysis of tissue samples in diagnosing and/or assessing the activity and/or developing a prognosis for and/or developing therapeutic options for said diseases.

29. (New) Method according to any one of claims 1 to 3, wherein said substances are employed in connection with selection of therapies for said diseases.